



ENTERED

PCT

# RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/914,549B

DATE: 01/29/2003 86

TIME: 15:03:35

Input Set : A:\Sequence Listing 914,549.txt

Output Set: N:\CRF4\01292003\I914549B.raw

3 <110> APPLICANT: Poustka, et al.  
5 <120> TITLE OF INVENTION: PROTEIN (TP) THAT IS INVOLVED IN THE DEVELOPMENT OF THE  
NERVOUS SYSTEM

7 <130> FILE REFERENCE: 4121-129

9 <140> CURRENT APPLICATION NUMBER: 09/914,549B

C--> 10 <141> CURRENT FILING DATE: 2002-08-14

12 <150> PRIOR APPLICATION NUMBER: PCT/DE00/00583

13 <151> PRIOR FILING DATE: 2000-02-28

15 <150> PRIOR APPLICATION NUMBER: DE 199 08 423.8

16 <151> PRIOR FILING DATE: 1999-02-26

18 <160> NUMBER OF SEQ ID NOS: 39

20 <170> SOFTWARE: PatentIn version 3.1

22 <210> SEQ ID NO: 1

23 <211> LENGTH: 242

24 <212> TYPE: DNA

25 <213> ORGANISM: Homo sapiens

27 <220> FEATURE:

28 <221> NAME/KEY: CDS

29 <222> LOCATION: (3)..(242)

30 <223> OTHER INFORMATION:

W--> 32 <400> 1

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| 33 | ag cga gtt act cac gct tcc cct cca tcg gaa gcc agc cag gcc aaa  | 47  |
| 34 | Arg Val Thr His Ala Ser Pro Pro Ser Glu Ala Ser Gln Ala Lys     |     |
| 35 | 1 5 10 15   |     |
| 37 | acc cag caa gat atg cag tcc agt ctg gca gcc aga tat gca act cag | 95  |
| 38 | Thr Gln Gln Asp Met Gln Ser Ser Leu Ala Ala Arg Tyr Ala Thr Gln |     |
| 39 | 20 25 30  |     |
| 41 | tct aat cac agt gga att gca acc agt caa aaa aag cct act agg ctt | 143 |
| 42 | Ser Asn His Ser Gly Ile Ala Thr Ser Gln Lys Lys Pro Thr Arg Leu |     |
| 43 | 35 40 45  |     |
| 45 | cca ggg ccc tct agg gtg cct gct gca gga agc agc agc aag gtc cag | 191 |
| 46 | Pro Gly Pro Ser Arg Val Pro Ala Ala Gly Ser Ser Ser Lys Val Gln |     |
| 47 | 50 55 60  |     |
| 49 | gga gcc tct aat tta aat agg aga agt cag agc ttt aac agc att gac | 239 |
| 50 | Gly Ala Ser Asn Leu Asn Arg Arg Ser Gln Ser Phe Asn Ser Ile Asp |     |
| 51 | 65 70 75  |     |
| 53 | aaa   | 242 |
| 54 | Lys   |     |
| 55 | 80  |     |
| 58 | <210> SEQ ID NO: 2  |     |
| 59 | <211> LENGTH: 80  |     |
| 60 | <212> TYPE: PRT   |     |
| 61 | <213> ORGANISM: Homo sapiens                                    |     |
| 63 | <400> SEQUENCE: 2   |     |

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```

65 Arg Val Thr His Ala Ser Pro Pro Ser Glu Ala Ser Gln Ala Lys Thr
66 1          5          10          15
69 Gln Gln Asp Met Gln Ser Ser Leu Ala Ala Arg Tyr Ala Thr Gln Ser
70          20          25          30
73 Asn His Ser Gly Ile Ala Thr Ser Gln Lys Lys Pro Thr Arg Leu Pro
74          35          40          45
77 Gly Pro Ser Arg Val Pro Ala Ala Gly Ser Ser Ser Lys Val Gln Gly
78          50          55          60
81 Ala Ser Asn Leu Asn Arg Arg Ser Gln Ser Phe Asn Ser Ile Asp Lys
82 65          70          75          80

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85 &lt;210&gt; SEQ ID NO: 3

86 &lt;211&gt; LENGTH: 159

87 &lt;212&gt; TYPE: DNA

88 &lt;213&gt; ORGANISM: Homo sapiens

90 &lt;220&gt; FEATURE:

91 &lt;221&gt; NAME/KEY: CDS

92 &lt;222&gt; LOCATION: (1)..(159)

93 &lt;223&gt; OTHER INFORMATION:

W--&gt; 95 &lt;400&gt; 3

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96 ggc act cac gag gtc cag agc ctg ctc atg aga acg ggt agt gtg aga      48
97 Gly Thr His Glu Val Gln Ser Leu Leu Met Arg Thr Gly Ser Val Arg
98 1          5          10          15
100 tct act ctc tca gaa aga tat acc cca tca tct cgg cag gcc aac caa      96
101 Ser Thr Leu Ser Glu Arg Tyr Thr Pro Ser Ser Arg Gln Ala Asn Gln
102          20          25          30
104 gaa gag ggc aaa gag tgg ttg cgt tct cat tct act gga ggg ctt cag      144
105 Glu Glu Gly Lys Glu Trp Leu Arg Ser His Ser Thr Gly Gly Leu Gln
106          35          40          45
108 gac act ggc aac cag      159
109 Asp Thr Gly Asn Gln
110          50

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113 &lt;210&gt; SEQ ID NO: 4

114 &lt;211&gt; LENGTH: 53

115 &lt;212&gt; TYPE: PRT

116 &lt;213&gt; ORGANISM: Homo sapiens

118 &lt;400&gt; SEQUENCE: 4

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120 Gly Thr His Glu Val Gln Ser Leu Leu Met Arg Thr Gly Ser Val Arg
121 1          5          10          15
124 Ser Thr Leu Ser Glu Arg Tyr Thr Pro Ser Ser Arg Gln Ala Asn Gln
125          20          25          30
128 Glu Glu Gly Lys Glu Trp Leu Arg Ser His Ser Thr Gly Gly Leu Gln
129          35          40          45
132 Asp Thr Gly Asn Gln
133          50

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136 &lt;210&gt; SEQ ID NO: 5

137 &lt;211&gt; LENGTH: 2461

138 &lt;212&gt; TYPE: DNA

139 &lt;213&gt; ORGANISM: Homo sapiens

141 &lt;220&gt; FEATURE:

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142 &lt;221&gt; NAME/KEY: CDS

143 &lt;222&gt; LOCATION: (2)..(1627)

144 &lt;223&gt; OTHER INFORMATION:

W--&gt; 146 &lt;400&gt; 5

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147 g gat cag ctt cgg gag acc atg cac aac atg cag ttg gag gtg gac ctg      49
148   Asp Gln Leu Arg Glu Thr Met His Asn Met Gln Leu Glu Val Asp Leu
149   1          5          10          15
151 ctg aaa gca gag aat gac cga ctg aag gta gcc cca ggc ccc tca tca      97
152 Leu Lys Ala Glu Asn Asp Arg Leu Lys Val Ala Pro Gly Pro Ser Ser
153   20          25          30
155 ggc tcc act cca ggg cag gtc cct gga tca tct gca tta tct tcc cca      145
156 Gly Ser Thr Pro Gly Gln Val Pro Gly Ser Ser Ala Leu Ser Ser Pro
157   35          40          45
159 cgc cgc tcc cta ggc ctg gca ctc acc cat tcc ttc ggc ccc agt ctt      193
160 Arg Arg Ser Leu Gly Leu Ala Leu Thr His Ser Phe Gly Pro Ser Leu
161   50          55          60
163 gca gac aca gac ctg tca ccc atg gat ggc atc agt act tgt ggt cca      241
164 Ala Asp Thr Asp Leu Ser Pro Met Asp Gly Ile Ser Thr Cys Gly Pro
165 65          70          75          80
167 aag gag gaa gtg acc ctc cgg gtg gtg gtg agg atg ccc ccg cag cac      289
168 Lys Glu Glu Val Thr Leu Arg Val Val Val Arg Met Pro Pro Gln His
169   85          90          95
171 atc atc aaa ggg gac ttg aag cag cag gaa ttc ttc ctg ggc tgt agc      337
172 Ile Ile Lys Gly Asp Leu Lys Gln Glu Phe Phe Leu Gly Cys Ser
173 100          105          110
175 aag gtc agt gga aaa gtt gac tgg aag atg ctg gat gaa gct gtt ttc      385
176 Lys Val Ser Gly Lys Val Asp Trp Lys Met Leu Asp Glu Ala Val Phe
177 115          120          125
179 caa gtg ttc aag gac tat att tct aaa atg gac cca gcc tct acc ctg      433
180 Gln Val Phe Lys Asp Tyr Ile Ser Lys Met Asp Pro Ala Ser Thr Leu
181 130          135          140
183 gga cta agc act gag tcc atc cat ggc tac agc atc agc cac gtg aaa      481
184 Gly Leu Ser Thr Glu Ser Ile His Gly Tyr Ser Ile Ser His Val Lys
185 145          150          155          160
187 cga gtg ttg gat gca gag ccc ccc gag atg cct cct tgc cgt cga ggt      529
188 Arg Val Leu Asp Ala Glu Pro Pro Glu Met Pro Pro Cys Arg Arg Gly
189   165          170          175
191 gtc aat aac ata tca gtc tcc ctc aaa ggt ctg aag gag aaa tgc gtc      577
192 Val Asn Asn Ile Ser Val Ser Leu Lys Gly Leu Lys Glu Lys Cys Val
193 180          185          190
195 gac agc ctg gtg ttc gag acg ctg atc ccc aag ccg atg atg cag cac      625
196 Asp Ser Leu Val Phe Glu Thr Leu Ile Pro Lys Pro Met Met Gln His
197 195          200          205
199 tac ata agc ctc ctg ctg aag cac cgg cgc ctc gtc ctc tgc ggc ccc      673
200 Tyr Ile Ser Leu Leu Leu Lys His Arg Arg Leu Val Leu Ser Gly Pro
201 210          215          220
203 agc ggc acg ggc aag acc tac ctg acc aat cgc ttg gcc gag tac ctg      721
204 Ser Gly Thr Gly Lys Thr Tyr Leu Thr Asn Arg Leu Ala Glu Tyr Leu
205 225          230          235          240

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 207 | gtg | gag | cgc | tct | ggc | cgt | gag | gtc | aca | gag | ggc | atc | gtc | agc | acc | ttc | 769  |
| 208 | Val | Glu | Arg | Ser | Gly | Arg | Glu | Val | Thr | Glu | Gly | Ile | Val | Ser | Thr | Phe |      |
| 209 |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |      |
| 211 | aac | atg | cac | cag | cag | tct | tgc | aag | gat | ctg | caa | ctg | tat | ctt | tcc | aac | 817  |
| 212 | Asn | Met | His | Gln | Gln | Ser | Cys | Lys | Asp | Leu | Gln | Leu | Tyr | Leu | Ser | Asn |      |
| 213 |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |
| 215 | cta | gcc | aac | cag | ata | gac | cgg | gaa | aca | gga | att | ggg | gat | gtg | ccc | ctg | 865  |
| 216 | Leu | Ala | Asn | Gln | Ile | Asp | Arg | Glu | Thr | Gly | Ile | Gly | Asp | Val | Pro | Leu |      |
| 217 |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| 219 | gtg | att | cta | ttg | gat | gac | ctg | agt | gaa | gca | ggc | tcc | atc | agt | gag | ttg | 913  |
| 220 | Val | Ile | Leu | Leu | Asp | Asp | Leu | Ser | Glu | Ala | Gly | Ser | Ile | Ser | Glu | Leu |      |
| 221 |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| 223 | gtc | aat | ggg | gcc | ctc | acc | tgc | aag | tat | cat | aaa | tgt | ccc | tat | att | ata | 961  |
| 224 | Val | Asn | Gly | Ala | Leu | Thr | Cys | Lys | Tyr | His | Lys | Cys | Pro | Tyr | Ile | Ile |      |
| 225 | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |      |
| 227 | ggt | acc | acc | aat | cag | cct | gta | aaa | atg | aca | ccc | aac | cat | ggc | ttg | cac | 1009 |
| 228 | Gly | Thr | Thr | Asn | Gln | Pro | Val | Lys | Met | Thr | Pro | Asn | His | Gly | Leu | His |      |
| 229 |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |     |      |
| 231 | ttg | agc | ttc | agg | atg | ttg | acc | ttc | tcc | aac | aac | gtg | gag | cca | gcc | aat | 1057 |
| 232 | Leu | Ser | Phe | Arg | Met | Leu | Thr | Phe | Ser | Asn | Asn | Val | Glu | Pro | Ala | Asn |      |
| 233 |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |
| 235 | ggc | ttc | ctg | gtt | cgt | tac | ctg | agg | agg | aag | ctg | gta | gag | tca | gac | agc | 1105 |
| 236 | Gly | Phe | Leu | Val | Arg | Tyr | Leu | Arg | Lys | Leu | Val | Glu | Ser | Asp | Ser |     |      |
| 237 |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| 239 | gac | atc | aat | gcc | aac | aag | gaa | gag | ctg | ctt | cgg | gtg | ctc | gac | tgg | gta | 1153 |
| 240 | Asp | Ile | Asn | Ala | Asn | Lys | Glu | Glu | Leu | Leu | Arg | Val | Leu | Asp | Trp | Val |      |
| 241 |     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| 243 | ccc | aag | ctg | tgg | tat | cat | ctc | cac | acc | ttc | ctt | gag | aag | cac | agc | acc | 1201 |
| 244 | Pro | Lys | Leu | Trp | Tyr | His | Leu | His | Thr | Phe | Leu | Glu | Lys | His | Ser | Thr |      |
| 245 | 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |
| 247 | tca | gac | ttc | ctc | atc | ggc | cct | tgc | ttc | ttt | ctg | tcg | tgt | ccc | att | ggc | 1249 |
| 248 | Ser | Asp | Phe | Leu | Ile | Gly | Pro | Cys | Phe | Phe | Leu | Ser | Cys | Pro | Ile | Gly |      |
| 249 |     |     |     | 405 |     |     |     |     |     | 410 |     |     |     | 415 |     |     |      |
| 251 | att | gag | gac | ttc | cgg | acc | tgg | ttc | att | gac | ctg | tgg | aac | aac | tct | atc | 1297 |
| 252 | Ile | Glu | Asp | Phe | Arg | Thr | Trp | Phe | Ile | Asp | Leu | Trp | Asn | Asn | Ser | Ile |      |
| 253 |     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
| 255 | att | ccc | tat | cta | cag | gaa | gga | gcc | aag | gat | ggg | ata | aag | gtc | cat | gga | 1345 |
| 256 | Ile | Pro | Tyr | Leu | Gln | Glu | Gly | Ala | Lys | Asp | Gly | Ile | Lys | Val | His | Gly |      |
| 257 |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |
| 259 | cag | aaa | gct | gct | tgg | gag | gac | cca | gtg | gaa | tgg | gtc | cgg | gac | aca | ctt | 1393 |
| 260 | Gln | Lys | Ala | Ala | Trp | Glu | Asp | Pro | Val | Glu | Trp | Val | Arg | Asp | Thr | Leu |      |
| 261 |     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |
| 263 | ccc | tgg | cca | tca | gcc | caa | caa | gac | caa | tca | aag | ctg | tac | cac | ctg | ccc | 1441 |
| 264 | Pro | Trp | Pro | Ser | Ala | Gln | Gln | Asp | Gln | Ser | Lys | Leu | Tyr | His | Leu | Pro |      |
| 265 | 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |      |
| 267 | cca | ccc | acc | gtg | ggc | cct | cac | agc | att | gcc | tca | cct | ccc | gag | gat | agg | 1489 |
| 268 | Pro | Pro | Thr | Val | Gly | Pro | His | Ser | Ile | Ala | Ser | Pro | Pro | Glu | Asp | Arg |      |
| 269 |     |     |     | 485 |     |     |     |     |     | 490 |     |     |     | 495 |     |     |      |
| 271 | aca | gtc | aaa | gac | agc | acc | cca | agt | tct | ctg | gac | tca | gat | cct | ctg | atg | 1537 |

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272 Thr Val Lys Asp Ser Thr Pro Ser Ser Leu Asp Ser Asp Pro Leu Met
273          500          505          510
275 gcc atg ctg ctg aaa ctt caa gaa gct gcc aac tac att gag tct cca 1585
276 Ala Met Leu Leu Lys Leu Gln Glu Ala Ala Asn Tyr Ile Glu Ser Pro
277          515          520          525
279 gat cga gaa acc atc ctg gac ccc aac ctt cag gca aca ctt 1627
280 Asp Arg Glu Thr Ile Leu Asp Pro Asn Leu Gln Ala Thr Leu
281          530          535          540
283 taagggttcg gcaatcactg tcacccccgg acagcagaac gctggcatca gctatcttag 1687
285 ctccctcctct cccctctcct ctttcagagc actggctctc cagccccagg aggagaacag 1747
287 gagggaggag gagatgaaag aggagggaca gggtcttggg gctgtacctt tgagaacttc 1807
289 ctaggaagga atggtggggg ggcgtttggg aacttgtgcc ccctaaacac atttactggc 1867
291 ctccctctaag gactttgggg aaaagatgat tctgggtctt tcccttgact tcttgtttca 1927
293 attacaaact cctgggcttt ctggggaggg gttcagaaaa catcaaaaca ctgcagcagt 1987
295 tcctaaatga ttctcacaag caaccctgag agagacagtc ttgtgaggga gatctggggg 2047
297 aggcaggaag ctctcagat tttctcacag acccttccca attccatcac cactgccaac 2107
299 aactcctccc ccagagatct ggctggagcc cagaaaaaga agcatgtggt ttaaaaaaatg 2167
301 tttaaataca tctgtaaaag gtaaaaatga aaaacaaaaa caagcaaaca aacaaaaaac 2227
303 aatggaaaag atgaagctgg agagagagga accagttgcc aaggtagaga gctgcccgt 2287
305 cctgccctct ggatgacata ggggacatca acaagacggc tgccaacctg agaagtcacc 2347
307 aaaccacaaa aataacctta cagccttcag ggaaagacta ccagctctgt ctttctacc 2407
309 tctaatttaa caatgcataa gagtcaataa accctacttt tttaaaaaaa aaaa 2461
312 <210> SEQ ID NO: 6
313 <211> LENGTH: 542
314 <212> TYPE: PRT
315 <213> ORGANISM: Homo sapiens
317 <400> SEQUENCE: 6
319 Asp Gln Leu Arg Glu Thr Met His Asn Met Gln Leu Glu Val Asp Leu
320 1          5          10          15
323 Leu Lys Ala Glu Asn Asp Arg Leu Lys Val Ala Pro Gly Pro Ser Ser
324          20          25          30
327 Gly Ser Thr Pro Gly Gln Val Pro Gly Ser Ser Ala Leu Ser Ser Pro
328          35          40          45
331 Arg Arg Ser Leu Gly Leu Ala Leu Thr His Ser Phe Gly Pro Ser Leu
332          50          55          60
335 Ala Asp Thr Asp Leu Ser Pro Met Asp Gly Ile Ser Thr Cys Gly Pro
336 65          70          75          80
339 Lys Glu Glu Val Thr Leu Arg Val Val Val Arg Met Pro Pro Gln His
340          85          90          95
343 Ile Ile Lys Gly Asp Leu Lys Gln Gln Glu Phe Phe Leu Gly Cys Ser
344          100          105          110
347 Lys Val Ser Gly Lys Val Asp Trp Lys Met Leu Asp Glu Ala Val Phe
348          115          120          125
351 Gln Val Phe Lys Asp Tyr Ile Ser Lys Met Asp Pro Ala Ser Thr Leu
352          130          135          140
355 Gly Leu Ser Thr Glu Ser Ile His Gly Tyr Ser Ile Ser His Val Lys
356 145          150          155          160
359 Arg Val Leu Asp Ala Glu Pro Pro Glu Met Pro Pro Cys Arg Arg Gly
360          165          170          175

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:39; N Pos. 109,6825,6842,6863

Seq#:39; N Pos. 80984,81012

**VERIFICATION SUMMARY**

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Input Set : A:\Sequence Listing 914,549.txt

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30  
L:95 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:93  
L:146 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:144  
L:465 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:463  
L:800 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:798  
L:873 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:871  
L:2642 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:2640  
L:3244 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:3242  
L:3260 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:3258  
L:4342 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:4340  
L:5623 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:5621  
L:5643 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:5641  
L:5663 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:5661  
L:5800 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:34,Line#:5798  
L:5852 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35,Line#:5850  
L:5978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:60  
L:6202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:6780  
L:6204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:6840  
L:8674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:80940  
L:8676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:81000